



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:33 AM UTC

PDB ID : 3HNO / pdb_00003hno
Title : Crystal Structure of Pyrophosphate-dependent phosphofructokinase from Nitrosospira multiformis. Northeast Structural Genomics Consortium target id NmR42
Authors : Seetharaman, J.; Abashidze, M.; Sahdev, S.; Janjua, H.; Xiao, R.; Ciccocanti, C.; Foote, E.L.; Acton, T.B.; Rost, B.; Montelione, G.T.; Hunt, J.F.; Tong, L.; Northeast Structural Genomics Consortium (NESG)
Deposited on : 2009-05-31
Resolution : 2.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

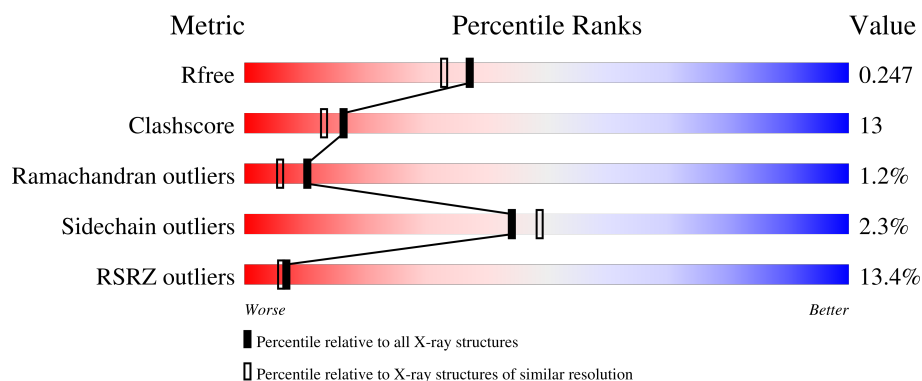
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	419	11% 76% 16% • 6%
1	B	419	9% 75% 17% • 6%
1	C	419	16% 73% 19% • 6%
1	D	419	14% 70% 22% • 6%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12308 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Pyrophosphate-dependent phosphofructokinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	395	Total	C	N	O	S	0	0	0
			2965	1886	502	562	15			
1	B	395	Total	C	N	O	S	0	0	0
			2965	1886	502	562	15			
1	C	395	Total	C	N	O	S	0	1	0
			2970	1890	502	562	16			
1	D	394	Total	C	N	O	S	0	1	0
			2966	1888	501	561	16			

- Molecule 2 is BROMIDE ION (CCD ID: BR) (formula: Br).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	1	Total	Br	0	0
			1	1		

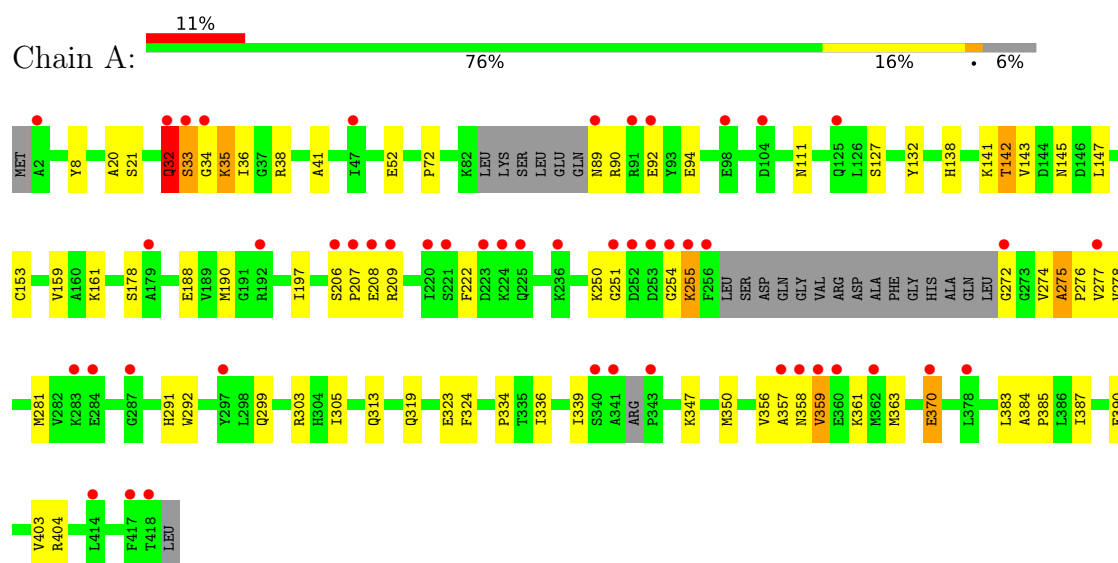
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	94	Total	O	0	0
			94	94		
3	B	130	Total	O	0	0
			130	130		
3	C	89	Total	O	0	0
			89	89		
3	D	128	Total	O	0	0
			128	128		

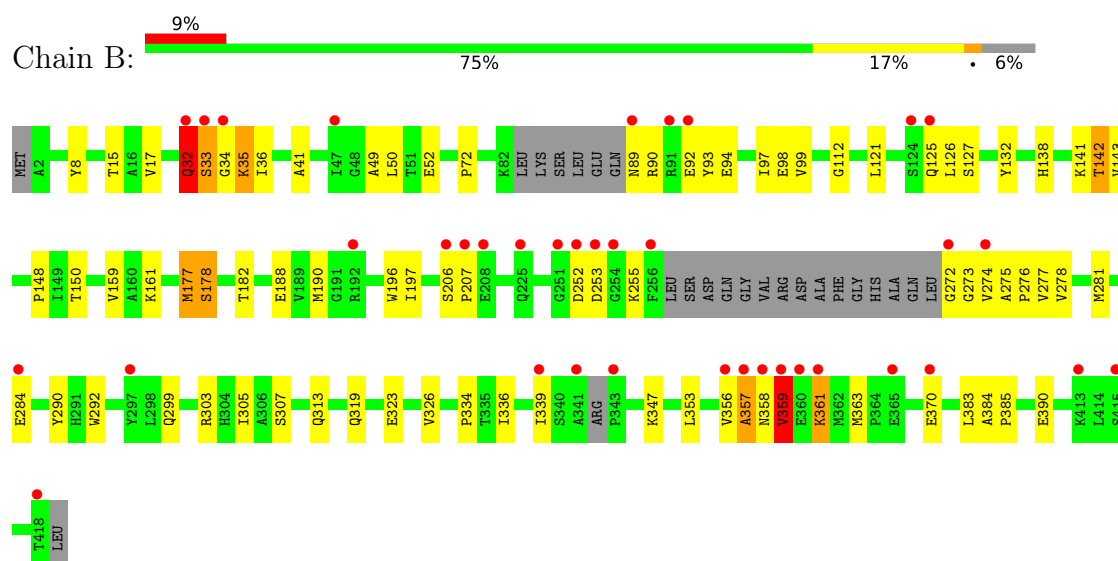
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Pyrophosphate-dependent phosphofructokinase

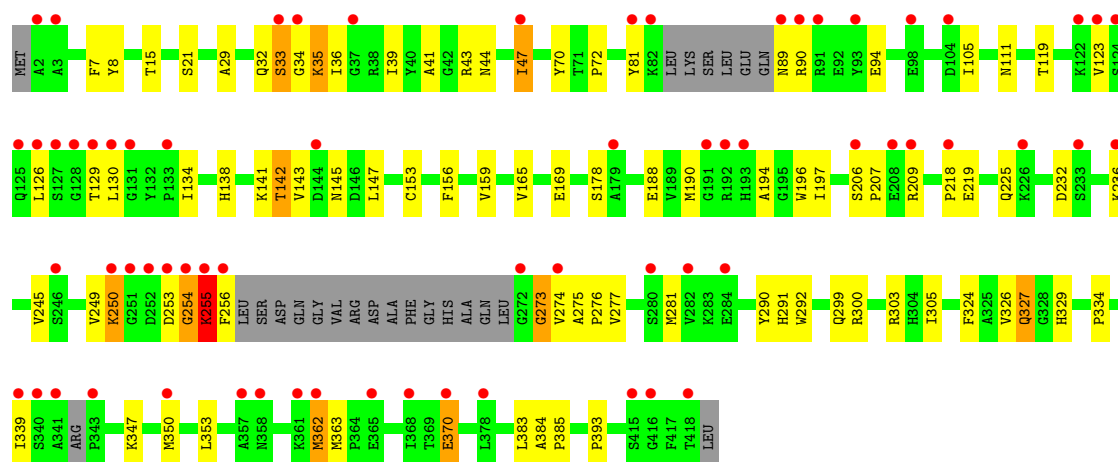


- Molecule 1: Pyrophosphate-dependent phosphofructokinase



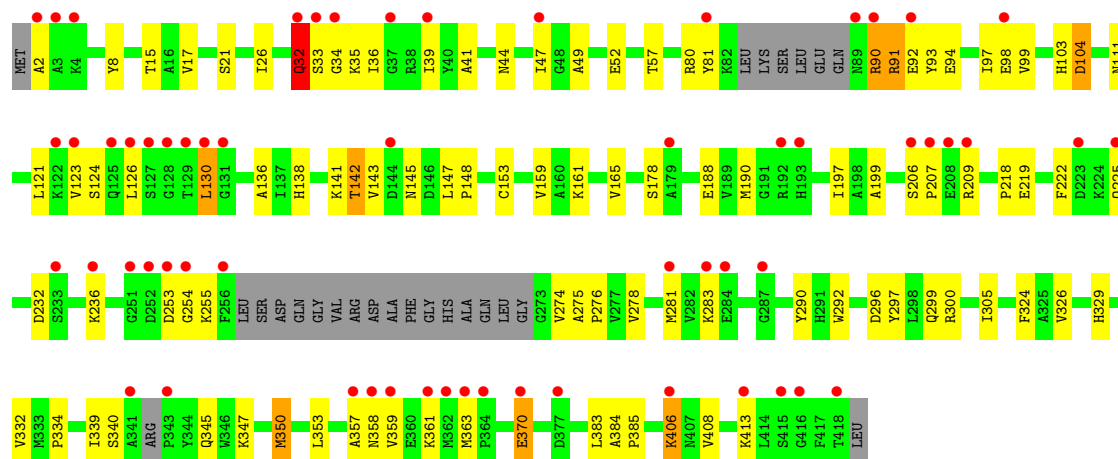
- Molecule 1: Pyrophosphate-dependent phosphofructokinase

Chain C: 



• Molecule 1: Pyrophosphate-dependent phosphofructokinase

Chain D: 



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	211.90Å 89.32Å 115.46Å 90.00° 119.12° 90.00°	Depositor
Resolution (Å)	39.45 – 2.00 39.45 – 2.00	Depositor EDS
% Data completeness (in resolution range)	94.7 (39.45-2.00) 95.2 (39.45-2.00)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.57 (at 1.90Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.216 , 0.241 0.221 , 0.247	Depositor DCC
R_{free} test set	11281 reflections (4.16%)	wwPDB-VP
Wilson B-factor (Å ²)	23.9	Xtriage
Anisotropy	0.610	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 44.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	12308	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.20% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: BR

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.41	1/3024 (0.0%)	0.86	7/4090 (0.2%)
1	B	0.50	1/3024 (0.0%)	0.89	10/4090 (0.2%)
1	C	0.40	0/3032	0.87	6/4100 (0.1%)
1	D	0.43	2/3028 (0.1%)	0.84	5/4095 (0.1%)
All	All	0.44	4/12108 (0.0%)	0.86	28/16375 (0.2%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	275	ALA	CA-CB	-6.75	1.42	1.53
1	B	253	ASP	CA-C	6.26	1.61	1.52
1	D	350[A]	MET	SD-CE	-5.43	1.66	1.79
1	D	350[B]	MET	SD-CE	-5.43	1.66	1.79

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	34	GLY	N-CA-C	-11.86	100.89	113.58
1	A	272	GLY	CA-C-N	-11.76	108.75	122.16
1	A	272	GLY	C-N-CA	-11.76	108.75	122.16
1	C	273	GLY	N-CA-C	-8.22	99.27	111.19
1	B	383	LEU	N-CA-C	8.14	119.93	111.14
1	C	383	LEU	N-CA-C	8.04	119.82	111.14
1	D	178	SER	N-CA-C	7.00	120.71	111.75
1	D	383	LEU	N-CA-C	6.67	118.35	111.14
1	A	178	SER	N-CA-C	6.47	119.15	111.71
1	B	35	LYS	N-CA-C	-6.46	105.42	113.55
1	B	178	SER	N-CA-C	6.44	119.99	111.75
1	B	273	GLY	N-CA-C	-6.34	98.16	113.18
1	A	383	LEU	N-CA-C	6.33	117.97	111.14

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	178	SER	N-CA-C	6.27	118.92	111.71
1	A	34	GLY	N-CA-C	-6.26	98.34	113.18
1	D	34	GLY	N-CA-C	-6.18	98.54	113.18
1	B	272	GLY	CA-C-N	-5.90	109.85	121.41
1	B	272	GLY	C-N-CA	-5.90	109.85	121.41
1	C	35	LYS	N-CA-C	-5.81	105.20	112.93
1	A	35	LYS	N-CA-C	-5.81	105.20	112.93
1	B	17	VAL	N-CA-C	5.80	117.76	112.43
1	B	34	GLY	N-CA-C	-5.79	99.45	113.18
1	D	17	VAL	N-CA-C	5.69	117.66	112.43
1	A	20	ALA	N-CA-C	-5.34	105.54	111.36
1	B	253	ASP	CA-C-N	5.26	131.72	121.41
1	B	253	ASP	C-N-CA	5.26	131.72	121.41
1	C	245	VAL	N-CA-C	5.16	115.33	108.11
1	D	26	ILE	N-CA-C	5.12	115.34	110.42

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2965	0	2931	74	0
1	B	2965	0	2931	66	0
1	C	2970	0	2940	84	0
1	D	2966	0	2937	82	0
2	C	1	0	0	0	0
3	A	94	0	0	0	0
3	B	130	0	0	1	0
3	C	89	0	0	2	0
3	D	128	0	0	5	0
All	All	12308	0	11739	306	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 13.

All (306) close contacts within the same asymmetric unit are listed below, sorted by their clash

magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:255:LYS:HA	1:C:255:LYS:CE	1.49	1.35
1:C:255:LYS:CA	1:C:255:LYS:HE3	1.52	1.31
1:D:332:VAL:HG21	1:D:350[A]:MET:HE2	1.20	1.19
1:C:250:LYS:HB3	1:C:254:GLY:HA2	1.41	1.03
1:D:278:VAL:HA	1:D:281:MET:HE2	1.46	0.95
1:A:278:VAL:HA	1:A:281:MET:HE3	1.52	0.92
1:A:190:MET:H	1:A:299:GLN:HE22	1.19	0.90
1:B:177:MET:HE3	1:B:177:MET:HA	1.57	0.87
1:B:358:ASN:O	1:B:359:VAL:HB	1.74	0.86
1:C:190:MET:H	1:C:299:GLN:HE22	1.23	0.85
1:C:255:LYS:HA	1:C:255:LYS:HE3	0.84	0.83
1:C:324:PHE:CG	1:C:350[A]:MET:HE3	2.14	0.82
1:D:190:MET:H	1:D:299:GLN:HE22	1.27	0.81
1:A:188:GLU:CD	1:A:274:VAL:HG12	2.06	0.81
1:B:190:MET:H	1:B:299:GLN:HE22	1.25	0.81
1:C:250:LYS:HD2	1:C:254:GLY:CA	2.10	0.81
1:C:255:LYS:HE3	1:C:255:LYS:C	2.05	0.81
1:D:332:VAL:HG21	1:D:350[A]:MET:CE	2.08	0.80
1:B:177:MET:HA	1:B:177:MET:CE	2.13	0.79
1:D:143:VAL:O	1:D:197:ILE:HD11	1.82	0.79
1:D:406:LYS:HD3	3:D:510:HOH:O	1.80	0.79
1:A:250:LYS:CG	1:A:255:LYS:H	1.95	0.78
1:D:324:PHE:CG	1:D:350[A]:MET:HE3	2.20	0.77
1:C:255:LYS:O	1:C:256:PHE:CB	2.34	0.74
1:C:143:VAL:O	1:C:197:ILE:HD11	1.86	0.74
1:A:89:ASN:HD22	1:A:92:GLU:HB2	1.51	0.74
1:C:206:SER:HB3	1:C:207:PRO:HD2	1.69	0.73
1:B:90:ARG:O	1:B:94:GLU:HG3	1.89	0.72
1:C:190:MET:HE2	1:C:299:GLN:CG	2.20	0.72
1:C:324:PHE:CD2	1:C:350[A]:MET:HE3	2.24	0.72
1:C:275:ALA:HB3	1:C:276:PRO:HD3	1.72	0.71
1:B:358:ASN:O	1:B:359:VAL:CB	2.38	0.70
1:A:159:VAL:HG11	1:A:197:ILE:HD12	1.73	0.70
1:D:324:PHE:CD2	1:D:350[A]:MET:HE3	2.26	0.70
1:D:283:LYS:HE3	1:D:290:TYR:CE2	2.27	0.69
1:A:250:LYS:CB	1:A:255:LYS:H	2.05	0.69
1:D:332:VAL:CG2	1:D:350[A]:MET:HE2	2.13	0.69
1:C:324:PHE:CG	1:C:350[A]:MET:CE	2.75	0.69
1:D:190:MET:HE2	1:D:299:GLN:HG3	1.75	0.69
1:B:35:LYS:HD3	1:B:326:VAL:HG13	1.75	0.68
1:C:327:GLN:HG2	3:D:544:HOH:O	1.94	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:250:LYS:HG2	1:A:255:LYS:H	1.58	0.67
1:C:324:PHE:CD1	1:C:350[A]:MET:HE3	2.29	0.67
1:A:190:MET:H	1:A:299:GLN:NE2	1.90	0.66
1:C:255:LYS:CE	1:C:255:LYS:CA	2.35	0.66
1:D:357:ALA:O	1:D:359:VAL:HG23	1.96	0.66
1:B:277:VAL:HG12	1:B:281:MET:HE2	1.78	0.65
1:A:188:GLU:OE1	1:A:274:VAL:HG12	1.95	0.65
1:D:124:SER:HB3	1:D:136:ALA:HB3	1.77	0.65
1:B:188:GLU:HB2	1:B:275:ALA:HB2	1.78	0.65
1:D:190:MET:HE2	1:D:299:GLN:CG	2.25	0.65
1:C:209:ARG:HH11	1:C:209:ARG:HG2	1.62	0.65
1:A:324:PHE:CD1	1:A:350:MET:HE2	2.33	0.64
1:C:32:GLN:HG2	1:C:326:VAL:HG21	1.79	0.64
1:B:89:ASN:HD22	1:B:92:GLU:HB2	1.61	0.64
1:A:188:GLU:HG3	1:A:274:VAL:CG1	2.28	0.64
1:B:159:VAL:HG11	1:B:197:ILE:HD12	1.80	0.63
1:D:15:THR:HG22	1:D:143:VAL:HG13	1.79	0.63
1:B:356:VAL:O	1:B:357:ALA:C	2.39	0.63
1:C:15:THR:HG22	1:C:143:VAL:HG13	1.81	0.62
1:A:250:LYS:HG2	1:A:255:LYS:N	2.15	0.62
1:B:206:SER:HB3	1:B:207:PRO:HD2	1.81	0.61
1:D:190:MET:HE1	1:D:300:ARG:HB3	1.81	0.61
1:A:143:VAL:O	1:A:197:ILE:HD11	1.99	0.61
1:D:94:GLU:O	1:D:98:GLU:HG3	2.01	0.61
1:C:276:PRO:HG3	1:C:292:TRP:CZ2	2.35	0.61
1:C:188:GLU:CD	1:C:274:VAL:HG12	2.26	0.61
1:D:384:ALA:HB3	1:D:385:PRO:HD3	1.82	0.61
1:D:206:SER:HB3	1:D:207:PRO:HD2	1.83	0.60
1:A:89:ASN:HD22	1:A:92:GLU:CB	2.13	0.60
1:D:209:ARG:HG2	1:D:209:ARG:HH11	1.67	0.60
1:C:126:LEU:O	1:C:130:LEU:HG	2.02	0.60
1:C:190:MET:HE2	1:C:299:GLN:HG3	1.85	0.59
1:B:190:MET:H	1:B:299:GLN:NE2	1.97	0.59
1:D:190:MET:H	1:D:299:GLN:NE2	1.97	0.59
1:C:339:ILE:HD11	1:C:347:LYS:HG2	1.85	0.59
1:B:339:ILE:HD11	1:B:347:LYS:HE3	1.84	0.59
1:D:329:HIS:CG	1:D:350[A]:MET:HE1	2.38	0.59
1:A:206:SER:HB3	1:A:207:PRO:HD2	1.85	0.59
1:C:32:GLN:HG3	1:C:35:LYS:HB2	1.85	0.58
1:C:250:LYS:HD2	1:C:254:GLY:C	2.28	0.58
1:A:89:ASN:HB3	1:A:92:GLU:HB3	1.85	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:89:ASN:HD22	1:B:92:GLU:CB	2.16	0.58
1:B:305:ILE:HG13	1:B:305:ILE:O	2.04	0.58
1:C:190:MET:H	1:C:299:GLN:NE2	1.98	0.58
1:D:275:ALA:HB3	1:D:276:PRO:HD3	1.86	0.58
1:A:250:LYS:HB3	1:A:254:GLY:HA2	1.85	0.57
1:C:254:GLY:O	1:C:255:LYS:HB2	2.04	0.57
1:A:358:ASN:OD1	1:A:359:VAL:N	2.38	0.57
1:B:94:GLU:O	1:B:98:GLU:HG3	2.04	0.57
1:D:32:GLN:HG2	1:D:326:VAL:HG21	1.85	0.57
1:C:190:MET:HE1	1:C:300:ARG:HB3	1.86	0.57
1:C:209:ARG:HG2	1:C:209:ARG:NH1	2.21	0.56
1:B:277:VAL:HG12	1:B:281:MET:CE	2.37	0.55
1:D:35:LYS:HD3	1:D:326:VAL:HG13	1.89	0.55
1:A:324:PHE:CE1	1:A:350:MET:HE2	2.41	0.55
1:C:250:LYS:HD2	1:C:254:GLY:HA3	1.86	0.55
1:D:2:ALA:HB3	1:D:104:ASP:OD1	2.07	0.55
1:B:143:VAL:O	1:B:197:ILE:HD11	2.06	0.55
1:B:159:VAL:CG1	1:B:197:ILE:HD12	2.36	0.55
1:C:35:LYS:HD3	1:C:326:VAL:HG13	1.88	0.55
1:B:148:PRO:HB3	1:B:359:VAL:HG12	1.89	0.54
1:A:339:ILE:HD11	1:A:347:LYS:HG2	1.88	0.54
1:D:90:ARG:O	1:D:94:GLU:HG3	2.06	0.54
1:A:356:VAL:O	1:A:358:ASN:O	2.26	0.54
1:B:276:PRO:HG3	1:B:292:TRP:CZ2	2.42	0.54
1:C:232:ASP:O	1:C:236:LYS:HG2	2.08	0.54
1:A:274:VAL:O	1:A:278:VAL:HG23	2.08	0.53
1:C:138:HIS:O	1:C:334:PRO:HD2	2.08	0.53
1:D:406:LYS:HE2	3:D:511:HOH:O	2.07	0.53
1:D:97:ILE:HG13	1:D:130:LEU:HD22	1.91	0.53
1:A:324:PHE:CG	1:A:350:MET:HE2	2.43	0.53
1:B:190:MET:HG3	1:B:299:GLN:CD	2.33	0.53
1:D:35:LYS:HE2	1:D:35:LYS:HA	1.91	0.53
1:D:209:ARG:HG2	1:D:209:ARG:NH1	2.23	0.53
1:B:89:ASN:HB3	1:B:92:GLU:HB3	1.91	0.53
1:C:190:MET:HG3	1:C:299:GLN:CD	2.34	0.53
1:B:275:ALA:HB3	1:B:276:PRO:HD3	1.90	0.53
1:A:52:GLU:O	1:A:52:GLU:HG2	2.08	0.53
1:D:143:VAL:HB	1:D:159:VAL:HG21	1.90	0.53
1:A:159:VAL:CG1	1:A:197:ILE:HD12	2.38	0.52
1:B:138:HIS:O	1:B:334:PRO:HD2	2.09	0.52
1:C:197:ILE:HG12	3:C:452:HOH:O	2.10	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:123:VAL:O	1:D:126:LEU:HB2	2.10	0.52
1:C:218:PRO:HD2	1:C:219:GLU:OE1	2.09	0.52
1:C:194:ALA:HB1	1:C:196:TRP:CD1	2.45	0.52
1:D:406:LYS:HB2	1:D:406:LYS:NZ	2.25	0.51
1:A:319:GLN:O	1:A:323:GLU:HG3	2.10	0.51
1:B:121:LEU:HD13	1:B:353:LEU:HB2	1.92	0.51
1:B:370:GLU:H	1:B:370:GLU:CD	2.19	0.51
1:C:324:PHE:CD2	1:C:350[A]:MET:CE	2.94	0.51
1:C:159:VAL:HG11	1:C:197:ILE:HD12	1.93	0.51
1:D:161:LYS:NZ	1:D:305:ILE:HD11	2.26	0.51
1:D:370:GLU:CD	1:D:370:GLU:H	2.19	0.51
1:B:319:GLN:O	1:B:323:GLU:HG3	2.11	0.51
1:D:138:HIS:O	1:D:334:PRO:HD2	2.11	0.51
1:C:277:VAL:HG12	1:C:281:MET:CE	2.40	0.50
1:D:91:ARG:HG3	3:D:423:HOH:O	2.10	0.50
1:B:32:GLN:O	1:B:33:SER:O	2.29	0.50
1:B:89:ASN:N	3:B:462:HOH:O	2.44	0.50
1:B:177:MET:CE	1:B:177:MET:CA	2.86	0.50
1:B:278:VAL:HA	1:B:281:MET:HE3	1.94	0.50
1:D:406:LYS:HE3	1:D:408:VAL:CG2	2.41	0.50
1:C:329:HIS:CD2	1:C:350[A]:MET:HE1	2.47	0.50
1:C:126:LEU:HB2	3:C:470:HOH:O	2.12	0.50
1:D:218:PRO:HD2	1:D:219:GLU:OE1	2.12	0.50
1:B:276:PRO:HG3	1:B:292:TRP:CH2	2.46	0.49
1:B:356:VAL:O	1:B:357:ALA:O	2.30	0.49
1:D:296:ASP:CG	1:D:297:TYR:H	2.18	0.49
1:C:249:VAL:O	1:C:255:LYS:O	2.31	0.49
1:D:93:TYR:O	1:D:97:ILE:HG12	2.12	0.49
1:D:52:GLU:O	1:D:52:GLU:HG2	2.13	0.49
1:A:250:LYS:HD2	1:A:254:GLY:CA	2.43	0.49
1:B:161:LYS:NZ	1:B:305:ILE:HD11	2.28	0.49
1:C:143:VAL:HB	1:C:159:VAL:HG21	1.95	0.49
1:A:275:ALA:HB3	1:A:276:PRO:HD3	1.95	0.48
1:A:384:ALA:HB3	1:A:385:PRO:HD3	1.95	0.48
1:B:313:GLN:HB3	1:B:336:ILE:HD11	1.95	0.48
1:C:362:MET:SD	1:C:362:MET:N	2.82	0.48
1:D:159:VAL:HG11	1:D:197:ILE:HD12	1.95	0.48
1:D:188:GLU:HB2	1:D:275:ALA:HB2	1.95	0.48
1:A:188:GLU:HB2	1:A:275:ALA:HB2	1.94	0.48
1:B:196:TRP:CE3	1:B:363:MET:HE3	2.48	0.48
1:B:127:SER:HB2	1:B:132:TYR:O	2.14	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:370:GLU:CD	1:D:370:GLU:N	2.71	0.48
1:A:147:LEU:HB2	1:A:153:CYS:SG	2.54	0.48
1:A:370:GLU:CD	1:A:370:GLU:H	2.21	0.48
1:B:33:SER:HA	1:B:36:ILE:O	2.14	0.48
1:B:121:LEU:O	1:B:125:GLN:HG2	2.13	0.48
1:A:32:GLN:HG3	1:A:35:LYS:HB2	1.95	0.48
1:D:124:SER:CB	1:D:136:ALA:HB3	2.44	0.47
1:C:190:MET:HG3	1:C:299:GLN:OE1	2.14	0.47
1:D:49:ALA:O	1:D:99:VAL:HG21	2.14	0.47
1:D:283:LYS:HE3	1:D:290:TYR:HE2	1.77	0.47
1:A:138:HIS:O	1:A:334:PRO:HD2	2.14	0.47
1:C:33:SER:HA	1:C:36:ILE:O	2.15	0.47
1:D:199:ALA:CB	1:D:363:MET:HE1	2.45	0.47
1:D:276:PRO:HG3	1:D:292:TRP:CZ2	2.50	0.47
1:B:141:LYS:O	1:B:142:THR:HB	2.14	0.47
1:D:44:ASN:O	1:D:47:ILE:HG22	2.13	0.47
1:D:141:LYS:O	1:D:142:THR:HB	2.14	0.47
1:A:188:GLU:CG	1:A:274:VAL:CG1	2.93	0.47
1:A:276:PRO:HG3	1:A:292:TRP:CZ2	2.49	0.47
1:B:370:GLU:CD	1:B:370:GLU:N	2.73	0.46
1:C:70:TYR:HB2	1:C:393:PRO:HB3	1.98	0.46
1:A:250:LYS:CG	1:A:255:LYS:N	2.69	0.46
1:A:250:LYS:HD2	1:A:254:GLY:HA2	1.98	0.46
1:C:324:PHE:CE2	1:C:350[A]:MET:HE3	2.50	0.46
1:D:80:ARG:C	3:D:454:HOH:O	2.59	0.46
1:D:305:ILE:HG13	1:D:305:ILE:O	2.16	0.46
1:A:209:ARG:NH1	1:A:209:ARG:HG2	2.31	0.46
1:A:277:VAL:HG12	1:A:281:MET:HE2	1.96	0.46
1:C:90:ARG:O	1:C:94:GLU:HG3	2.15	0.46
1:D:32:GLN:O	1:D:33:SER:C	2.59	0.46
1:B:52:GLU:O	1:B:52:GLU:HG2	2.16	0.46
1:B:93:TYR:HB3	1:B:126:LEU:HD23	1.97	0.46
1:C:8:TYR:O	1:C:41:ALA:HA	2.16	0.46
1:B:390:GLU:N	1:B:390:GLU:CD	2.74	0.46
1:D:39:ILE:HB	1:D:57:THR:OG1	2.15	0.46
1:A:161:LYS:HE2	1:A:387:ILE:O	2.16	0.45
1:D:121:LEU:HD13	1:D:353:LEU:HB3	1.98	0.45
1:D:188:GLU:CD	1:D:274:VAL:HG12	2.41	0.45
1:C:370:GLU:CD	1:C:370:GLU:H	2.24	0.45
1:D:222:PHE:CZ	1:D:281:MET:HE1	2.51	0.45
1:D:406:LYS:HE3	1:D:408:VAL:HG23	1.97	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:222:PHE:HB3	1:A:251:GLY:HA2	1.97	0.45
1:A:370:GLU:CD	1:A:370:GLU:N	2.74	0.45
1:C:384:ALA:HB3	1:C:385:PRO:HD3	1.98	0.45
1:D:339:ILE:HD11	1:D:347:LYS:HD3	1.98	0.45
1:A:305:ILE:HG13	1:A:305:ILE:O	2.16	0.45
1:A:32:GLN:HB3	1:A:33:SER:H	1.62	0.45
1:B:93:TYR:O	1:B:97:ILE:HG12	2.16	0.45
1:B:384:ALA:HB3	1:B:385:PRO:HD3	1.98	0.45
1:C:165:VAL:O	1:C:169:GLU:HG3	2.16	0.45
1:A:141:LYS:O	1:A:142:THR:HB	2.16	0.45
1:A:188:GLU:CD	1:A:274:VAL:CG1	2.84	0.45
1:C:253:ASP:O	1:C:254:GLY:O	2.35	0.45
1:C:290:TYR:CD1	1:C:290:TYR:C	2.94	0.45
1:D:357:ALA:O	1:D:358:ASN:C	2.59	0.45
1:D:32:GLN:CG	1:D:326:VAL:HG21	2.47	0.45
1:C:43:ARG:O	1:C:44:ASN:HB2	2.16	0.44
1:D:8:TYR:O	1:D:41:ALA:HA	2.16	0.44
1:D:278:VAL:HA	1:D:281:MET:CE	2.33	0.44
1:C:138:HIS:CB	1:C:353:LEU:HD21	2.47	0.44
1:C:188:GLU:HB2	1:C:275:ALA:HB2	1.98	0.44
1:D:21:SER:HB2	1:D:111:ASN:HD21	1.81	0.44
1:A:250:LYS:HB3	1:A:255:LYS:H	1.80	0.44
1:D:290:TYR:CD1	1:D:290:TYR:C	2.96	0.44
1:A:90:ARG:HD2	1:A:94:GLU:CD	2.42	0.44
1:C:255:LYS:HA	1:C:255:LYS:NZ	2.21	0.44
1:D:141:LYS:O	1:D:141:LYS:HE2	2.18	0.44
1:C:119:THR:O	1:C:123:VAL:HG23	2.18	0.44
1:D:329:HIS:CD2	1:D:350[A]:MET:HE1	2.53	0.44
1:A:33:SER:HA	1:A:36:ILE:O	2.18	0.44
1:C:35:LYS:HE2	1:C:35:LYS:HA	1.99	0.44
1:C:141:LYS:O	1:C:142:THR:HB	2.18	0.44
1:C:370:GLU:CD	1:C:370:GLU:N	2.75	0.44
1:D:145:ASN:O	1:D:361:LYS:HE2	2.18	0.44
1:A:8:TYR:O	1:A:41:ALA:HA	2.18	0.43
1:B:89:ASN:ND2	1:B:92:GLU:N	2.66	0.43
1:B:148:PRO:CB	1:B:359:VAL:HG12	2.47	0.43
1:C:194:ALA:HB1	1:C:196:TRP:HD1	1.81	0.43
1:B:49:ALA:O	1:B:99:VAL:HG21	2.19	0.43
1:C:254:GLY:O	1:C:255:LYS:CB	2.64	0.43
1:D:147:LEU:HB2	1:D:153:CYS:SG	2.58	0.43
1:B:89:ASN:ND2	1:B:92:GLU:H	2.15	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:305:ILE:HG13	1:C:305:ILE:O	2.19	0.43
1:D:254:GLY:O	1:D:255:LYS:HB3	2.18	0.43
1:C:36:ILE:HG21	1:C:39:ILE:CD1	2.49	0.43
1:A:313:GLN:HB3	1:A:336:ILE:HD11	2.01	0.43
1:B:178:SER:HA	1:B:182:THR:O	2.18	0.43
1:B:188:GLU:CD	1:B:274:VAL:HG12	2.43	0.43
1:B:290:TYR:CD1	1:B:290:TYR:C	2.97	0.43
1:C:72:PRO:HB3	1:C:303:ARG:HB2	2.01	0.43
1:A:190:MET:HG3	1:A:299:GLN:CD	2.44	0.43
1:B:112:GLY:O	1:B:138:HIS:HE1	2.02	0.43
1:A:90:ARG:O	1:A:94:GLU:HG3	2.18	0.43
1:B:15:THR:HG22	1:B:143:VAL:HG13	2.00	0.43
1:B:50:LEU:HD21	1:B:92:GLU:HG3	2.01	0.42
1:A:390:GLU:CD	1:A:390:GLU:N	2.77	0.42
1:B:90:ARG:HD2	1:B:94:GLU:OE2	2.19	0.42
1:C:188:GLU:OE1	1:C:274:VAL:HG12	2.19	0.42
1:D:33:SER:HA	1:D:36:ILE:O	2.19	0.42
1:A:21:SER:HB2	1:A:111:ASN:HD21	1.85	0.42
1:B:190:MET:HG3	1:B:299:GLN:OE1	2.18	0.42
1:C:324:PHE:CE1	1:C:350[A]:MET:HE3	2.55	0.42
1:A:208:GLU:HG3	1:A:209:ARG:HG3	2.00	0.42
1:D:161:LYS:O	1:D:165:VAL:HG23	2.20	0.42
1:A:32:GLN:O	1:A:33:SER:OG	2.35	0.42
1:C:147:LEU:HB2	1:C:153:CYS:SG	2.60	0.42
1:A:72:PRO:HB3	1:A:303:ARG:HB2	2.02	0.42
1:A:356:VAL:O	1:A:357:ALA:C	2.63	0.42
1:C:89:ASN:OD1	1:C:90:ARG:N	2.52	0.42
1:D:340:SER:HB3	1:D:345:GLN:OE1	2.19	0.42
1:B:8:TYR:O	1:B:41:ALA:HA	2.20	0.42
1:B:72:PRO:HB3	1:B:303:ARG:HB2	2.01	0.41
1:C:47:ILE:HD11	1:C:81:TYR:CD1	2.54	0.41
1:A:127:SER:HB2	1:A:132:TYR:O	2.20	0.41
1:A:305:ILE:O	1:A:305:ILE:HG23	2.20	0.41
1:C:7:PHE:HB2	1:C:105:ILE:HD13	2.02	0.41
1:C:277:VAL:HG12	1:C:281:MET:HE3	2.02	0.41
1:A:38:ARG:HG2	1:A:38:ARG:HH11	1.85	0.41
1:A:276:PRO:HG3	1:A:292:TRP:CH2	2.55	0.41
1:B:150:THR:O	1:B:361:LYS:HE3	2.20	0.41
1:A:358:ASN:CG	1:A:359:VAL:H	2.28	0.41
1:A:250:LYS:HG2	1:A:255:LYS:CA	2.51	0.41
1:B:161:LYS:HD2	1:B:307:SER:HA	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:148:PRO:HD3	1:D:359:VAL:O	2.21	0.41
1:D:161:LYS:HZ3	1:D:305:ILE:HD11	1.84	0.41
1:A:209:ARG:HG2	1:A:209:ARG:HH11	1.85	0.41
1:A:250:LYS:HG2	1:A:255:LYS:HA	2.03	0.41
1:D:103:HIS:CE1	1:D:413:LYS:HD3	2.56	0.41
1:D:276:PRO:HG3	1:D:292:TRP:CH2	2.56	0.41
1:A:254:GLY:O	1:A:255:LYS:CB	2.69	0.41
1:A:403:VAL:HG22	1:A:404:ARG:N	2.36	0.41
1:C:196:TRP:CZ3	1:C:363:MET:HE3	2.56	0.41
1:C:29:ALA:HB1	1:C:39:ILE:HD11	2.02	0.40
1:D:232:ASP:O	1:D:236:LYS:HG2	2.21	0.40
1:B:177:MET:HE3	1:B:177:MET:CA	2.37	0.40
1:C:21:SER:HB2	1:C:111:ASN:HD21	1.87	0.40
1:C:145:ASN:HB2	1:C:156:PHE:CG	2.56	0.40
1:A:324:PHE:CZ	1:A:350:MET:HE2	2.57	0.40
1:C:273:GLY:O	1:C:277:VAL:HG23	2.22	0.40
1:D:81:TYR:HE2	1:D:92:GLU:OE1	2.04	0.40
1:A:143:VAL:HB	1:A:159:VAL:HG21	2.04	0.40
1:A:145:ASN:O	1:A:361:LYS:HE3	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	387/419 (92%)	366 (95%)	17 (4%)	4 (1%)	12	8
1	B	387/419 (92%)	369 (95%)	12 (3%)	6 (2%)	7	3
1	C	388/419 (93%)	368 (95%)	16 (4%)	4 (1%)	12	8
1	D	387/419 (92%)	364 (94%)	19 (5%)	4 (1%)	12	8
All	All	1549/1676 (92%)	1467 (95%)	64 (4%)	18 (1%)	10	6

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	357	ALA
1	B	359	VAL
1	C	255	LYS
1	A	32	GLN
1	A	33	SER
1	A	142	THR
1	B	33	SER
1	B	142	THR
1	C	142	THR
1	C	254	GLY
1	B	32	GLN
1	C	33	SER
1	D	32	GLN
1	D	142	THR
1	D	253	ASP
1	B	252	ASP
1	A	359	VAL
1	D	90	ARG

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	305/329 (93%)	300 (98%)	5 (2%)	55	62
1	B	305/329 (93%)	299 (98%)	6 (2%)	48	54
1	C	306/329 (93%)	296 (97%)	10 (3%)	33	34
1	D	306/329 (93%)	299 (98%)	7 (2%)	44	49
All	All	1222/1316 (93%)	1194 (98%)	28 (2%)	44	49

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	GLN
1	A	255	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	291	HIS
1	A	363	MET
1	A	370	GLU
1	B	32	GLN
1	B	177	MET
1	B	255	LYS
1	B	284	GLU
1	B	359	VAL
1	B	361	LYS
1	C	47	ILE
1	C	129	THR
1	C	134	ILE
1	C	225	GLN
1	C	250	LYS
1	C	255	LYS
1	C	291	HIS
1	C	327	GLN
1	C	362	MET
1	C	370	GLU
1	D	32	GLN
1	D	91	ARG
1	D	104	ASP
1	D	130	LEU
1	D	225	GLN
1	D	370	GLU
1	D	406	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	GLN
1	A	89	ASN
1	A	111	ASN
1	A	125	GLN
1	A	138	HIS
1	A	299	GLN
1	A	329	HIS
1	B	32	GLN
1	B	89	ASN
1	B	125	GLN
1	B	138	HIS
1	B	193	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	291	HIS
1	B	299	GLN
1	B	319	GLN
1	B	327	GLN
1	B	329	HIS
1	C	111	ASN
1	C	135	GLN
1	C	138	HIS
1	C	291	HIS
1	C	299	GLN
1	C	327	GLN
1	C	345	GLN
1	D	32	GLN
1	D	89	ASN
1	D	111	ASN
1	D	291	HIS
1	D	299	GLN
1	D	319	GLN
1	D	355	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	395/419 (94%)	0.69	48 (12%) 8 7	18, 29, 47, 55	0
1	B	395/419 (94%)	0.46	37 (9%) 14 13	15, 25, 44, 54	0
1	C	395/419 (94%)	0.97	66 (16%) 4 4	16, 30, 48, 59	1 (0%)
1	D	394/419 (94%)	0.75	60 (15%) 5 5	15, 27, 46, 58	1 (0%)
All	All	1579/1676 (94%)	0.72	211 (13%) 7 6	15, 28, 46, 59	2 (0%)

All (211) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	3	ALA	7.7
1	A	359	VAL	7.5
1	C	2	ALA	7.2
1	D	130	LEU	7.0
1	C	126	LEU	6.7
1	D	358	ASN	6.5
1	C	254	GLY	6.1
1	B	358	ASN	6.0
1	D	131	GLY	6.0
1	D	254	GLY	6.0
1	C	256	PHE	5.8
1	D	2	ALA	5.7
1	C	129	THR	5.6
1	C	90	ARG	5.5
1	D	126	LEU	5.5
1	D	256	PHE	5.5
1	D	92	GLU	5.3
1	A	254	GLY	5.3
1	A	253	ASP	5.2
1	C	3	ALA	5.2
1	D	89	ASN	5.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	127	SER	5.1
1	B	89	ASN	5.0
1	C	253	ASP	4.9
1	C	34	GLY	4.9
1	D	33	SER	4.9
1	A	92	GLU	4.8
1	B	357	ALA	4.8
1	A	358	ASN	4.8
1	C	252	ASP	4.8
1	C	362	MET	4.8
1	A	89	ASN	4.7
1	C	127	SER	4.7
1	A	206	SER	4.7
1	A	272	GLY	4.7
1	B	256	PHE	4.6
1	C	128	GLY	4.6
1	D	125	GLN	4.6
1	A	207	PRO	4.6
1	C	89	ASN	4.6
1	D	359	VAL	4.5
1	D	253	ASP	4.5
1	D	128	GLY	4.4
1	C	125	GLN	4.4
1	B	206	SER	4.4
1	C	280	SER	4.4
1	C	255	LYS	4.3
1	A	256	PHE	4.1
1	C	339	ILE	4.1
1	C	272	GLY	4.1
1	A	209	ARG	4.0
1	B	92	GLU	4.0
1	C	357	ALA	4.0
1	C	37	GLY	4.0
1	D	209	ARG	4.0
1	C	418	THR	3.9
1	B	359	VAL	3.9
1	B	284	GLU	3.9
1	A	252	ASP	3.9
1	D	90	ARG	3.9
1	C	206	SER	3.8
1	A	370	GLU	3.8
1	C	370	GLU	3.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	131	GLY	3.8
1	A	418	THR	3.8
1	B	252	ASP	3.8
1	C	33	SER	3.7
1	C	284	GLU	3.7
1	B	272	GLY	3.6
1	D	34	GLY	3.6
1	D	225	GLN	3.6
1	A	255	LYS	3.5
1	A	33	SER	3.5
1	C	209	ARG	3.5
1	A	34	GLY	3.5
1	D	206	SER	3.5
1	B	418	THR	3.5
1	A	208	GLU	3.5
1	D	192	ARG	3.5
1	D	418	THR	3.5
1	D	341	ALA	3.4
1	D	98	GLU	3.4
1	D	129	THR	3.4
1	D	362	MET	3.4
1	D	47	ILE	3.4
1	C	341	ALA	3.3
1	A	362	MET	3.3
1	C	350[A]	MET	3.3
1	D	236	LYS	3.3
1	A	225	GLN	3.3
1	D	370	GLU	3.2
1	C	130	LEU	3.1
1	D	284	GLU	3.1
1	C	191	GLY	3.1
1	B	192	ARG	3.1
1	D	357	ALA	3.1
1	C	358	ASN	3.1
1	D	207	PRO	3.1
1	A	297	TYR	3.0
1	B	254	GLY	3.0
1	A	104	ASP	3.0
1	C	144	ASP	3.0
1	B	370	GLU	3.0
1	D	4	LYS	3.0
1	B	415	SER	2.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	220	ILE	2.9
1	C	208	GLU	2.9
1	B	341	ALA	2.9
1	D	208	GLU	2.9
1	A	223	ASP	2.8
1	D	252	ASP	2.8
1	A	378	LEU	2.8
1	B	413	LYS	2.8
1	C	415	SER	2.8
1	B	297	TYR	2.8
1	C	343	PRO	2.8
1	C	193	HIS	2.8
1	C	416	GLY	2.8
1	D	193	HIS	2.7
1	B	208	GLU	2.7
1	A	251	GLY	2.7
1	A	343	PRO	2.7
1	D	416	GLY	2.7
1	A	91	ARG	2.7
1	A	236	LYS	2.7
1	A	283	LYS	2.7
1	C	365	GLU	2.7
1	B	124	SER	2.7
1	D	123	VAL	2.7
1	B	253	ASP	2.7
1	B	361	LYS	2.7
1	A	125	GLN	2.6
1	D	415	SER	2.6
1	B	47	ILE	2.6
1	C	91	ARG	2.6
1	D	81	TYR	2.6
1	B	32	GLN	2.6
1	B	251	GLY	2.6
1	D	32	GLN	2.6
1	D	223	ASP	2.6
1	C	250	LYS	2.6
1	D	343	PRO	2.6
1	C	246	SER	2.6
1	C	226	LYS	2.5
1	B	125	GLN	2.5
1	C	378	LEU	2.5
1	D	37	GLY	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	413	LYS	2.5
1	B	34	GLY	2.5
1	C	361	LYS	2.5
1	D	364	PRO	2.5
1	D	281	MET	2.5
1	C	47	ILE	2.5
1	C	98	GLU	2.4
1	A	340	SER	2.4
1	C	133	PRO	2.4
1	D	122	LYS	2.4
1	D	361	LYS	2.4
1	A	192	ARG	2.4
1	B	360	GLU	2.4
1	C	93	TYR	2.4
1	C	192	ARG	2.4
1	C	236	LYS	2.4
1	A	287	GLY	2.4
1	C	251	GLY	2.4
1	A	417	PHE	2.4
1	B	225	GLN	2.4
1	B	33	SER	2.4
1	C	124	SER	2.4
1	C	81	TYR	2.3
1	A	360	GLU	2.3
1	D	363	MET	2.3
1	D	406	LYS	2.3
1	C	233	SER	2.3
1	B	207	PRO	2.3
1	A	414	LEU	2.3
1	C	82	LYS	2.3
1	A	341	ALA	2.3
1	A	179	ALA	2.3
1	C	104	ASP	2.3
1	D	233	SER	2.2
1	B	339	ILE	2.2
1	D	283	LYS	2.2
1	D	377	ASP	2.2
1	C	179	ALA	2.2
1	C	368	ILE	2.2
1	B	365	GLU	2.2
1	D	251	GLY	2.2
1	A	357	ALA	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	218	PRO	2.1
1	D	144	ASP	2.2
1	A	47	ILE	2.1
1	B	274	VAL	2.1
1	B	356	VAL	2.1
1	A	32	GLN	2.1
1	A	2	ALA	2.1
1	A	224	LYS	2.1
1	C	123	VAL	2.1
1	A	221	SER	2.1
1	C	274	VAL	2.1
1	C	282	VAL	2.1
1	B	343	PRO	2.1
1	D	39	ILE	2.1
1	A	277	VAL	2.1
1	A	284	GLU	2.0
1	C	340	SER	2.1
1	C	122	LYS	2.0
1	D	287	GLY	2.0
1	A	98	GLU	2.0
1	D	179	ALA	2.0
1	B	91	ARG	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [\(i\)](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [\(i\)](#)

There are no oligosaccharides in this entry.

6.4 Ligands [\(i\)](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	BR	C	500	1/1	0.97	0.30	30,30,30,30	0

6.5 Other polymers [i](#)

There are no such residues in this entry.